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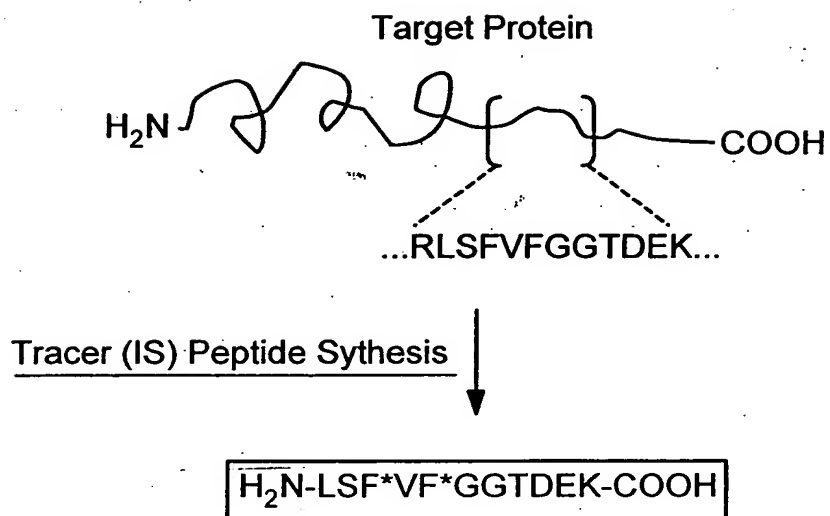


FIG. 1

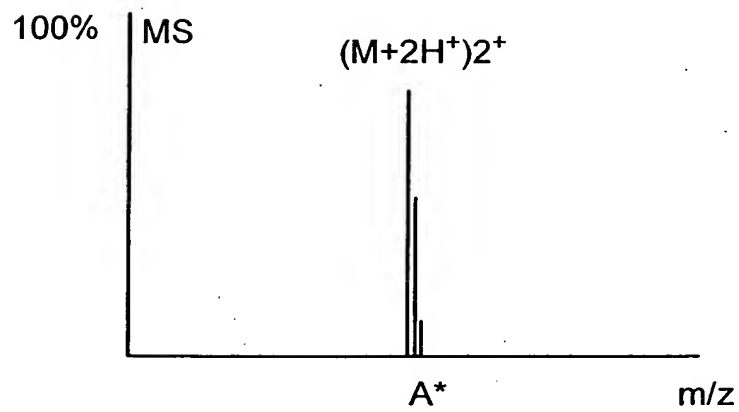


FIG. 2

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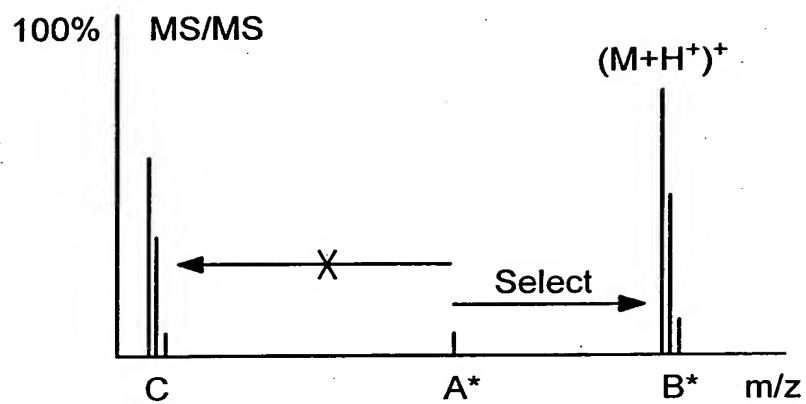


FIG. 3A.

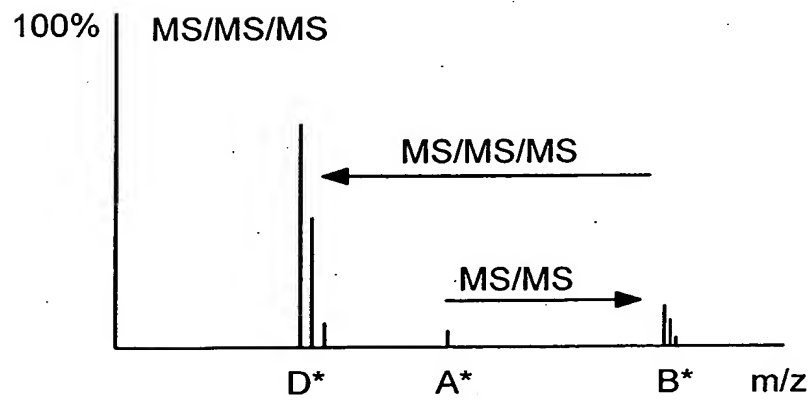


FIG. 3B

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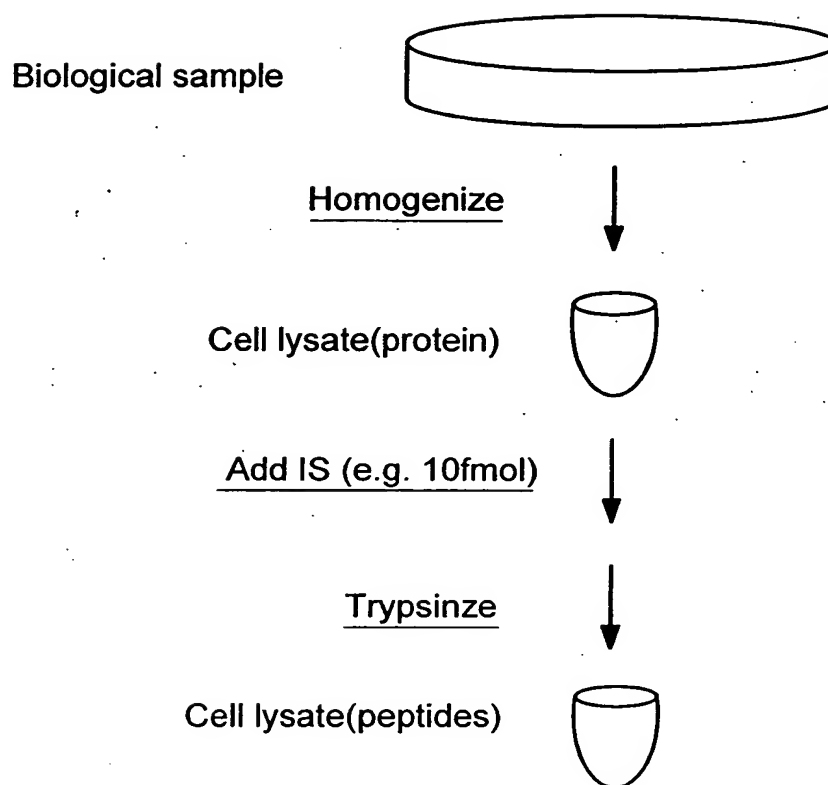


FIG. 4A

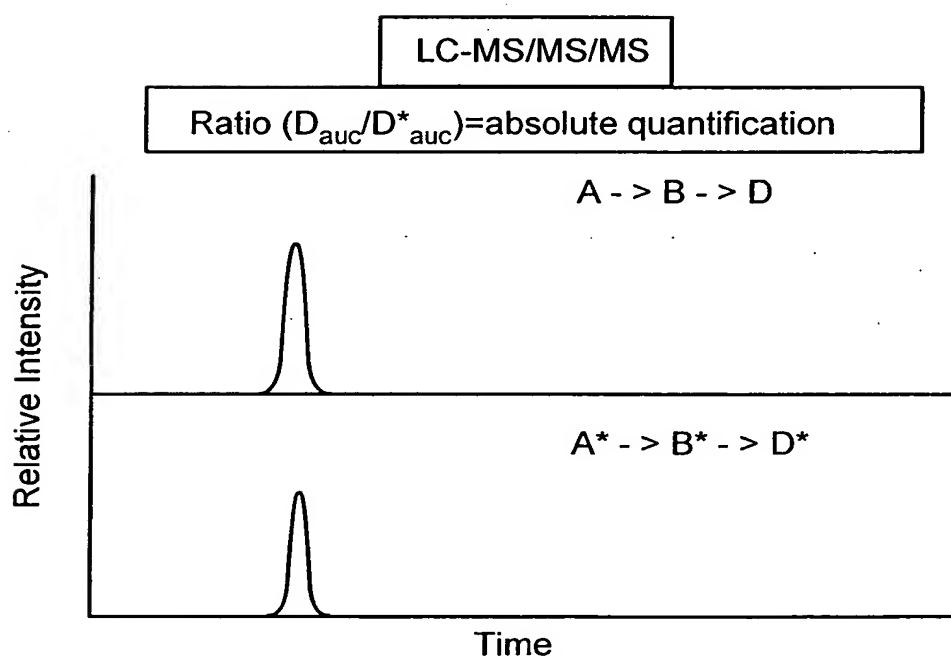
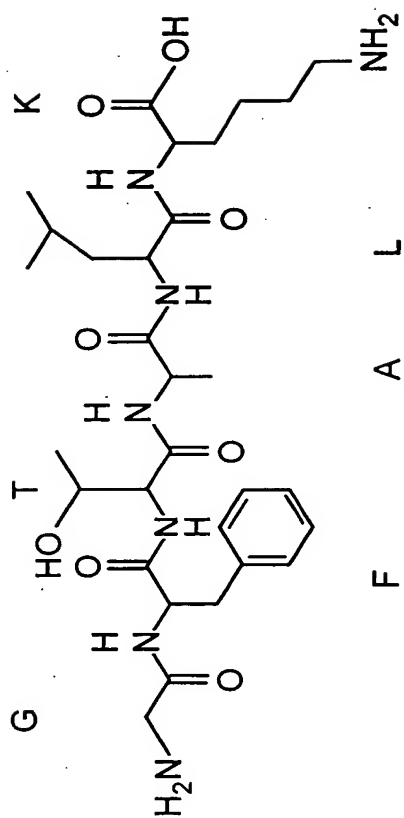


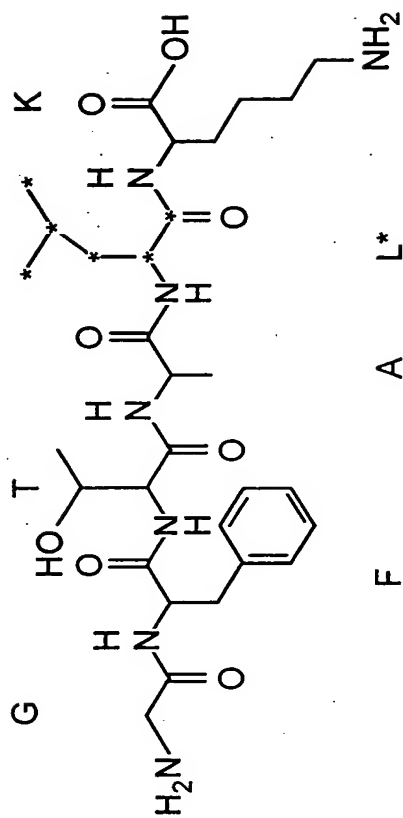
FIG. 4B



Native tryptic peptide

GFTALK

MW: 635.364



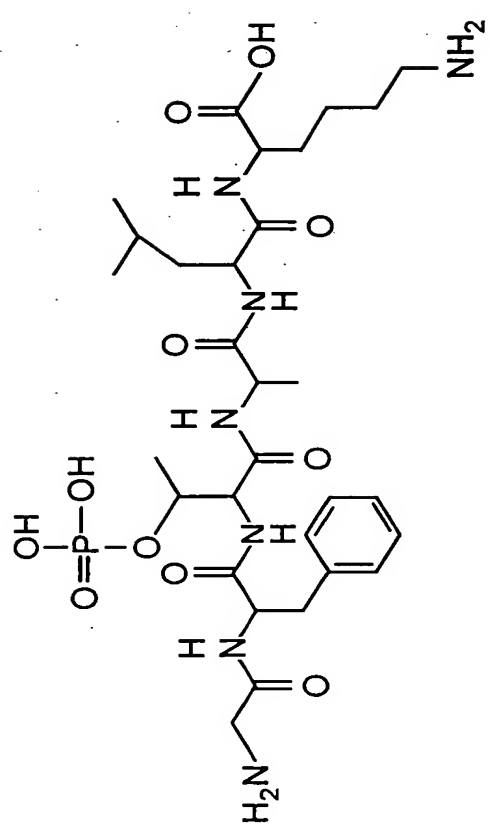
AQUA Internal Standard

GFTAL\*K

MW: 641.364

\* = stable isotope (e.g. <sup>13</sup>C)

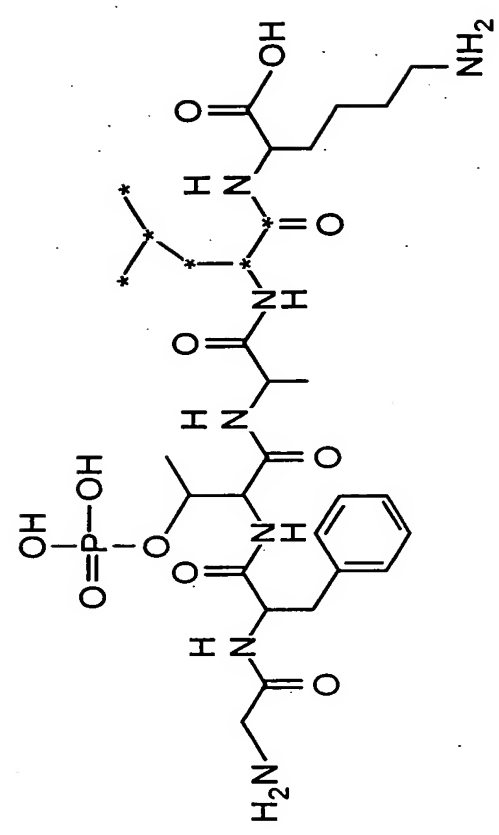
FIG. 5A



Native phosphopeptide

GF(pT)ALK

MW: 715.754



AQUA phosphopeptide  
Internal Standard

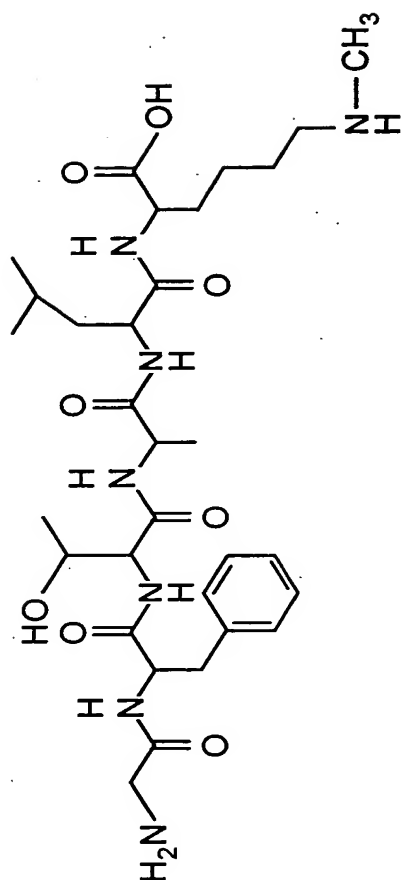
GF(pT)AL\*K

MW: 721.75

\* = stable isotope (e.g. <sup>13</sup>C)

FIG. 5B

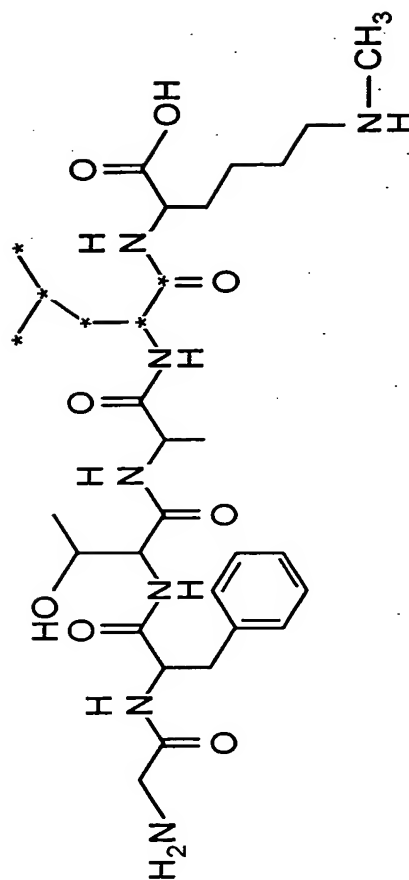
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Native methylated peptide

GFTAL(mK)

MW: 649.79

AQUA methylated peptide  
Internal Standard

GFTAL\*(mK)

MW: 655.79

\* = stable isotope (e.g.  $^{13}\text{C}$ )

FIG. 5C

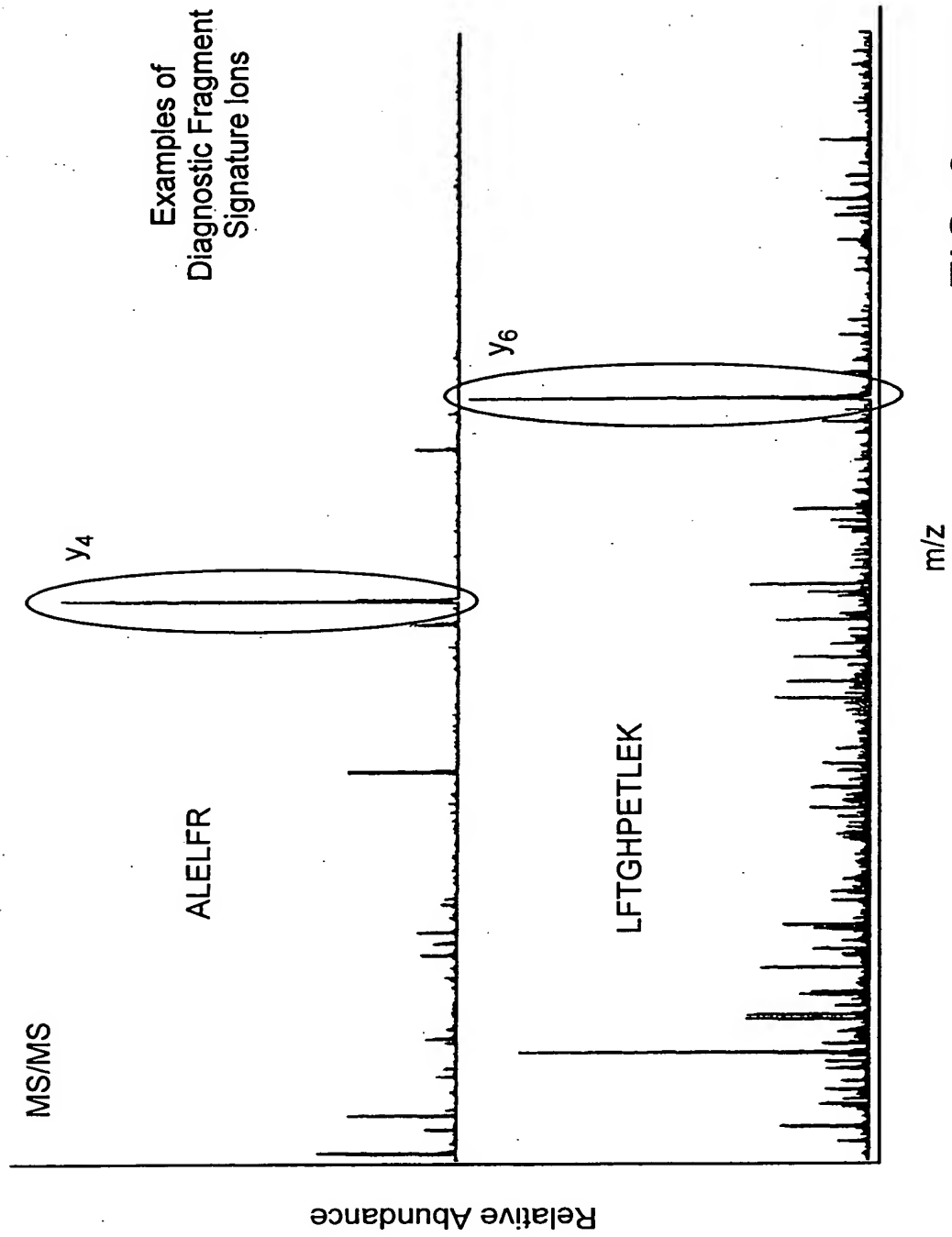


FIG. 6

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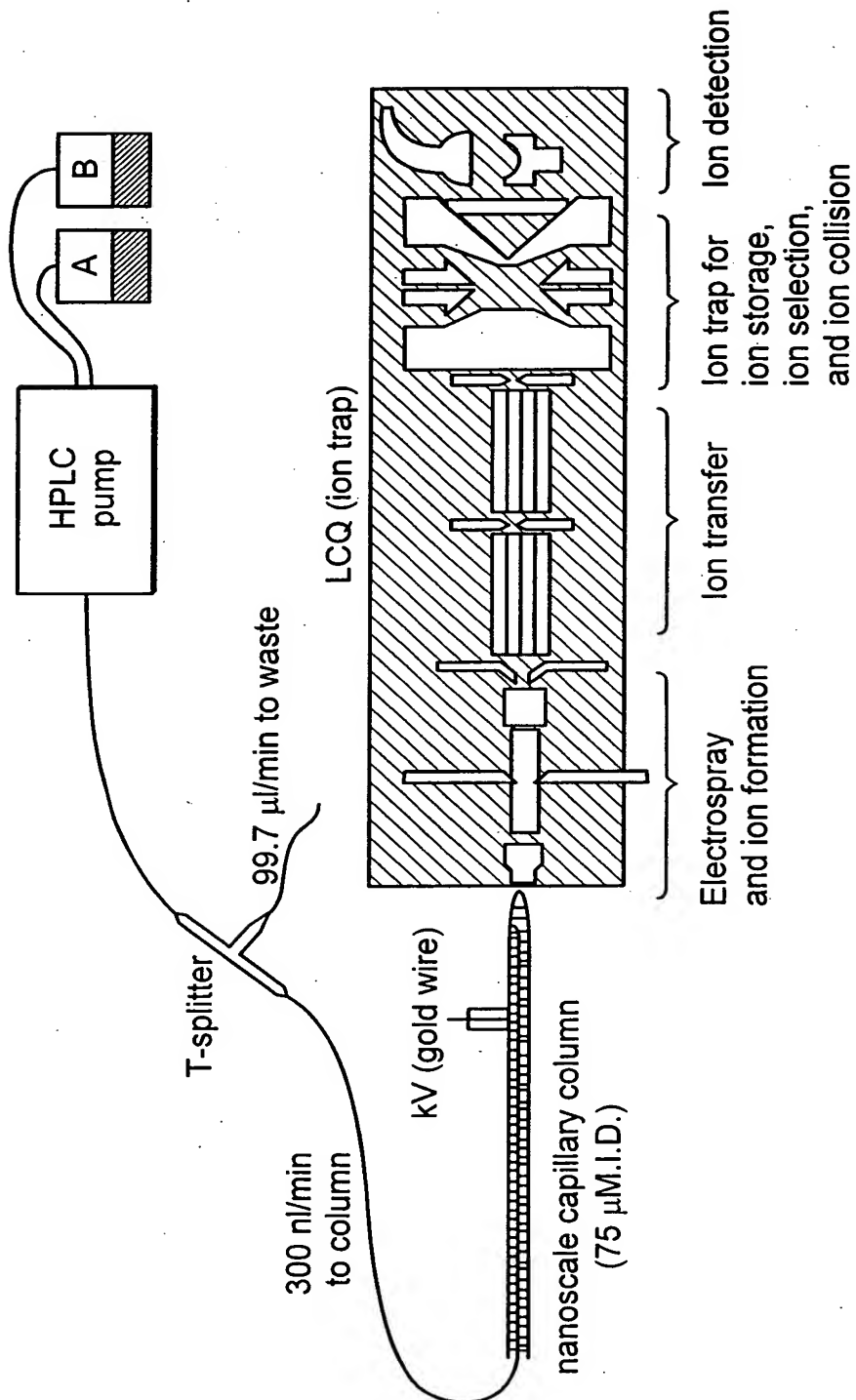


FIG. 7



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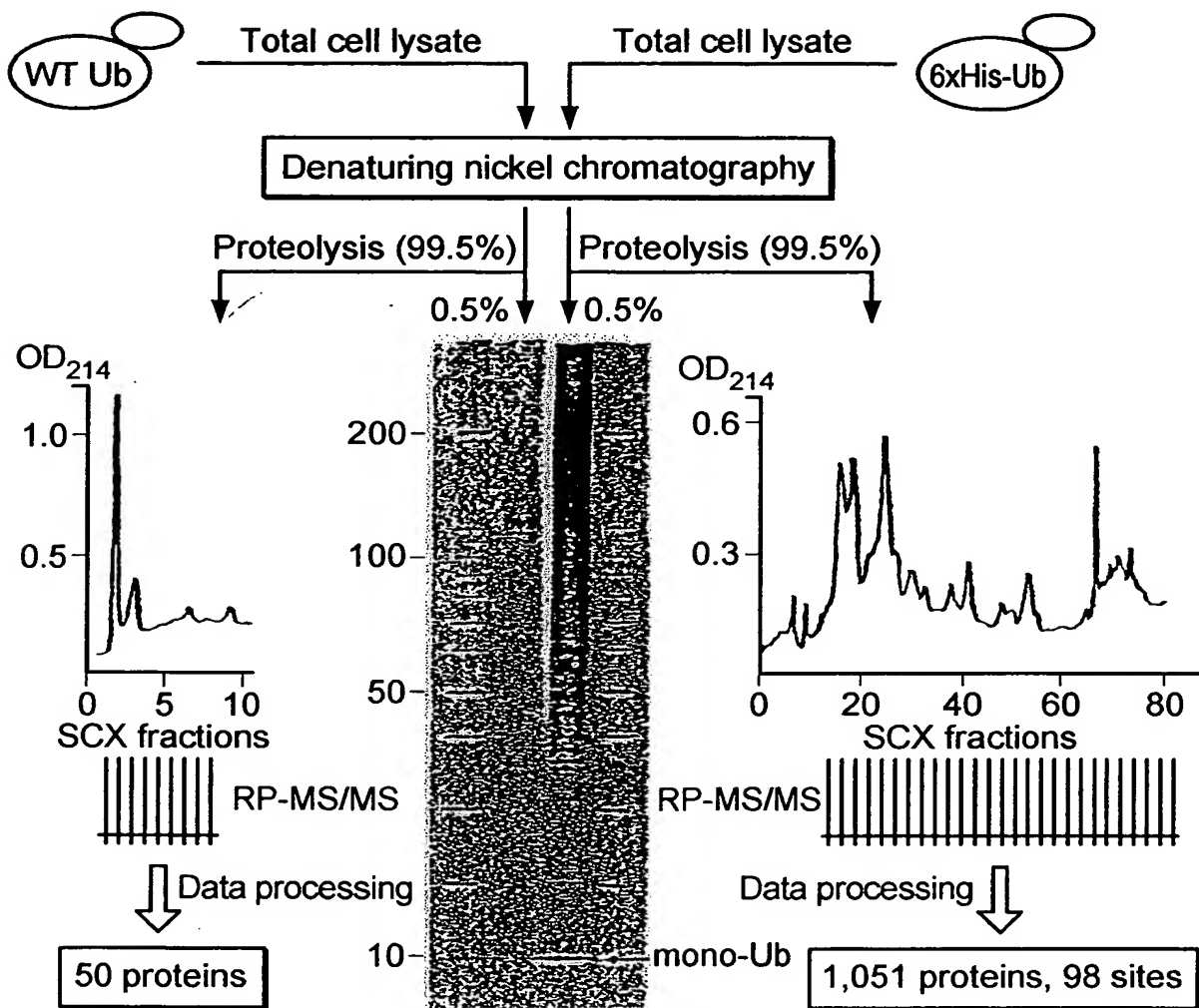


FIG. 8

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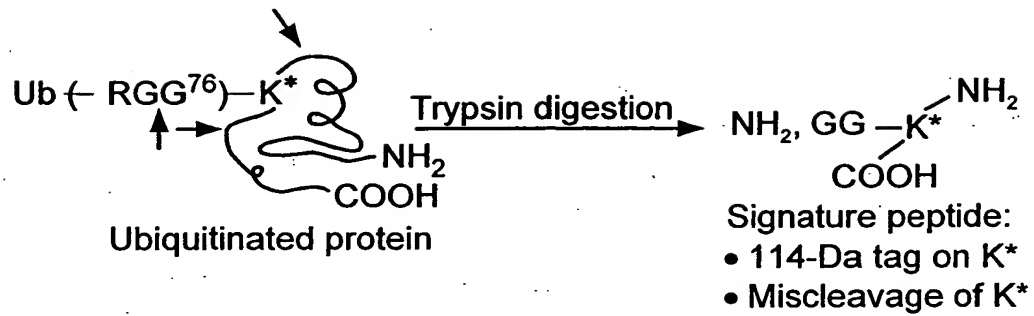


FIG. 9A

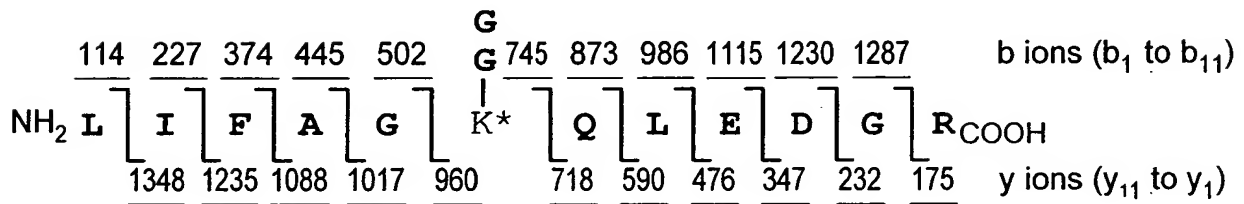


FIG. 9B

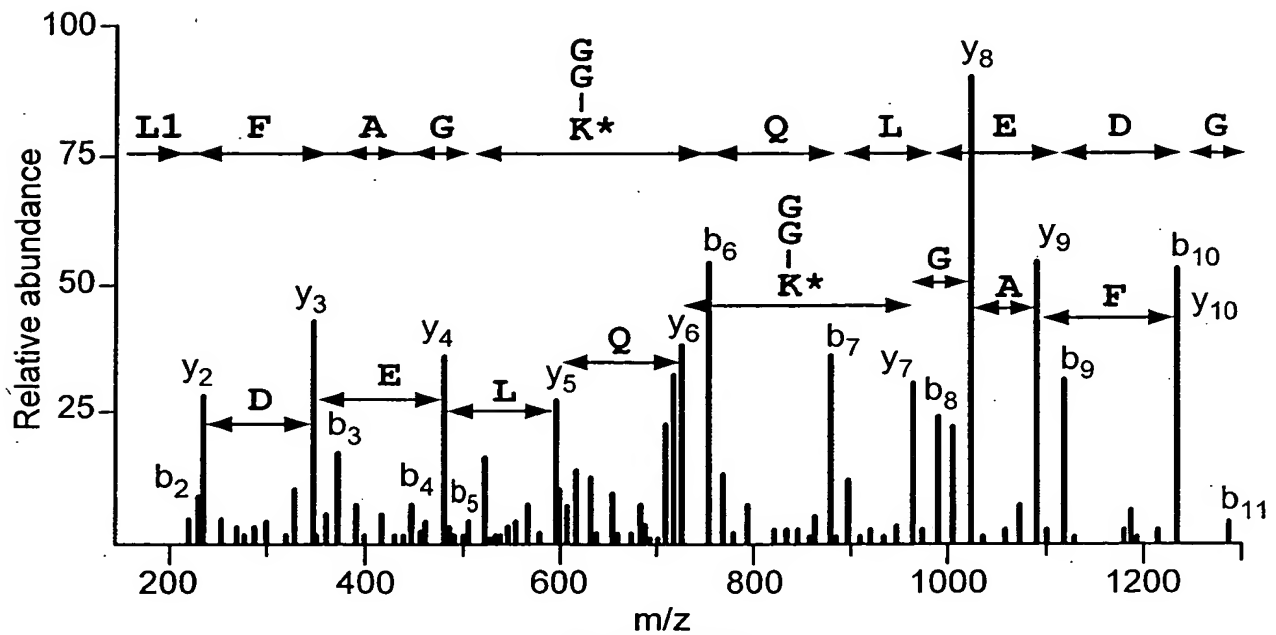


FIG. 9C

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Name	#sites	
Ubiquitin	5	MPFITSRPVA KNSSHSLSSET DLNQSKGQPF QPSPTKKLGS MQQRRRSSTI RHALSSLLGG
ECM21	5	ANVHSPAVLN NTTKGGNNNG NIRSSNIDAQ LLGKKQNKCP PPNARRHSTT AIQGSISDSA
SAM2	4	TTTPRSSTSD TNRTSGRLS VDQEPRISSG RYSQIEEDST VLDFDDDHNS SAVVSSDLSS
YHRD97C	3	TSLTRLANSK KFNEQFLIEY LTARGLLGPK TVLSNEYLKI SISTSGESVF LPTISSNDDE
HXT7	3	YLSRLNGLND GTDDAEADFF MDGIDQQEGN TPSLATATAA TESGGSINEN RDTLLRENN
GNP1	3	GDHPGSGSEL NTRSVEIDSS MVSYSIAVIV SVKKPTRFTD MQLELCNRVK VEVNTGVPPT
YILD41W	2	KTFNEEFYNA ASMKVNLNDE NFDLFVPLSI SPDGQMIENN SDRQVRLFK NIPTEERLYL
YHLD1DC	2	DKTKTKASLL NAIDVNKTHL YQPGDYVFLV PVVFSNHIPE TIYLP SARVS YRLRLATKAI
LSB1	2	NRKGFYRQDS NSPQPIVSPD SSSSLSTTS SLKLTETESA QAHRRISNTL FSKVKNLHM
ZE01	2	SSHQLKNEES GEEDIFAEYP IKVIRTPPPV AVSTANKPIY INRVWTDLS YEISFAQKYV
PHOM	2	SLNSEVPIKI KLAICKNVC VKRIHVSITE RVTFSKGYE YEYDQITPVA KDPYNPYLD
URA3	2	FASKRRKERS VSLFEIRTKG KTRALREEI VENSFNINLE SYSPFDDSD SKGNPKERLG
GDH1	2	ITEPIIIETK LKFPKYEDLD KRTAKIIPPY GIDAYTSIPN PEHAVANGPS HRRPSVIGFE
ERG5	2	SGHKGSKSHE ENKPVYDPK FHQDIKSNS GLPVKTHTRL NIPKRGYLD SLHFSNVYCR
ERG3	2	HKLEIMIRIS KPDPECPSKL RHYEVLIDTP IFLVSEQNS GNMELPTYDM ATMEGKGNQV
YGR26DC	2	PLSMNSDFFG NICPPPTEFE EAISVPASPI VSPMGSPNIM ASYDPDLIS QQLNLSRTTS
YMR295C	2	VSGPSGYSDD AGVPNVNRNS ISNANAMNGS ISNSAFVSGN SGQGVARARA TSVNDRSRFN
		NLDKLLSTPS PVNRSHNSSP TNGLSQANGT VRIPNATTEN SKDKQNEFFK KGYTLANVKD
		DEEQEGIVSS SSADSLLSHG NEPPRYDEIV PLMSDEE

FIG. 10A

Site in Ub (K)	Signature peptide	SCX fraction	Abundance
48	LIFAGK*QLEDGR	48-56 (9)	high
63	TLSDYNIQK*ESTLHLVLR	65-72 (8)	high
11	TLTGK*TITLEVESSDTIDNVK	38-42 (5)	medium
27	TITLEVESSDTIDNVK*SK	41 (1)	low
6	LISEEDLGMQIFVK*TLTGK	38 (1)	low

FIG. 10B

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Name	Phosphopeptide sequence	Description of function
ACC1	AVS*VSDLSYVANSQSSPLR	Acetyl.CoA carboxylase
CCC1	GSGGTSELGGSEST*PLLR	Protein potentially in calcium regulation
CHO1	DENDGYAS*DEVGGTLR	Phosphatidylserine synthase
CHS1	DDEYDDLNT*IDK	Chitin synthase I
CHS3	NPSTLLPTS*SMFWNK	Chitin synthase III
ECM21	NEES*GEEDIFAEYPIK	Protein possibly in cell wall biosynthesis
	HALSS*LLGGANVHSPAVLNNTTK	
	RPS*VIGFLSGHK	
	S*HNSS*PTNGLSQANGTVR	
GCD6	EEIDS*EFEDEDFEK	Translation initiation factor eIF2B
HSP3D	ASGETAIHEPEPEAEQAVEDT*A	Heat shock protein located in cell membrane
LYP1	LQVVSHT*DINEDEEEAHYEDK	High affinity lysine specific permease
MET4	KYS*DNEDEYDDADLHGFEK	Transcriptional activator
MYO3	RGS*VYHVPLNPVQATAVR	Myosine type I
PHO84	IHDT*S*DEDMAINGLER	Inorganic phosphate/H <sup>+</sup> symporter
	NNDIESSS*PSQLQHEA	
RAD16	SVNYNELS*DDDTAVK	Nucleotide excision repair protein
Ubiquitin	TLS*DYNIQK	Protein for posttranslational modification
YDR119W	IEEINENS*PLLSAPSK	Member of major facilitator superfamily (MFS)
YDR348C	TNS*FDMPQLNTR	Protein of unknown function
YHR097C	ETVDDDSET*LNQLQDR	Protein of unknown function
	LPSYEEAAGT*PK	
YOR042W	KNPDEDEFLINS*DDEM	Protein of unknown function
	SSGIDEDEVVT*PAEDAKEEEEEHPPLPAR	
	EQHHEDS*EEEDSWSQFVEK	
YPL019C	HYIADLEDHES*S*DEEGTALPK	Vacuolar polyphosphate accumulation

FIG. 10C

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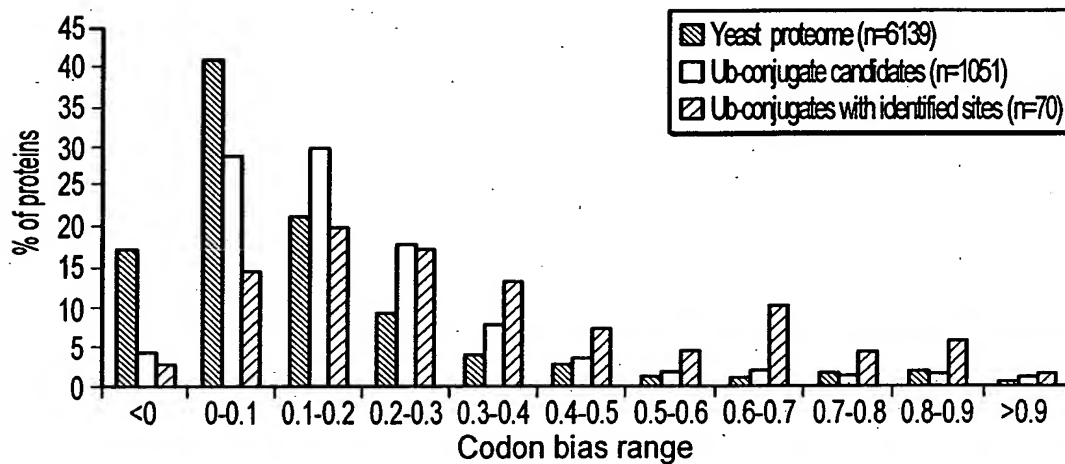


FIG. 11A

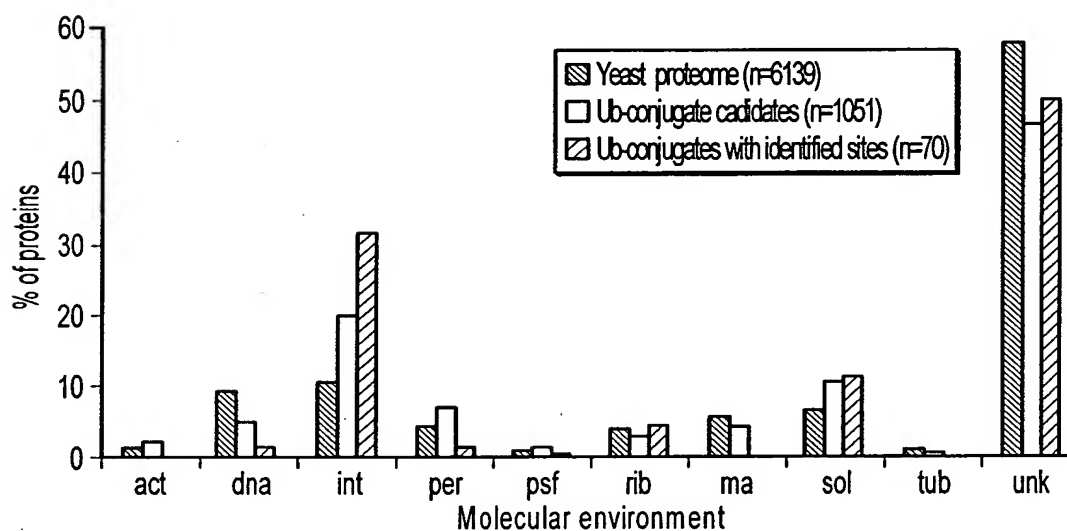


FIG. 11B

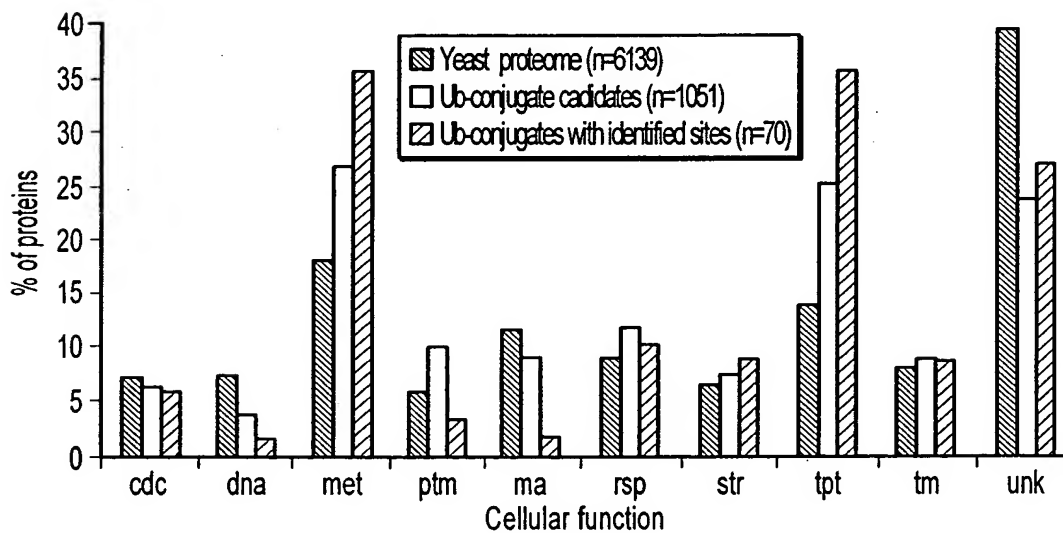


FIG. 11C